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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES

Ex parte SIMA THERAPEUTICS, INC.,
Patent Owner and Appellant

Appeal 2009-002562
Reexamination Control 90/008,177
Patent 7,022,828
Technology Center 3900

Decided:¹ May 26, 2009

Before CAROL A. SPIEGEL, ROMULO H. DELMENDO, and
JEFFREY FREDMAN, *Administrative Patent Judges*.

SPIEGEL, *Administrative Patent Judge*.

DECISION ON APPEAL

I. Statement of the Case

Appellant appeals under 35 U.S.C. §§ 134(b) and 306 from an Examiner's final rejection of all pending claims, claims 1-9 and 14-16.² We have jurisdiction under 35 U.S.C. §§ 134(b) and 306. We AFFIRM.

¹ The two-month for filing an appeal or commencing a civil action, as recited in 37 C.F.R. § 1.304, begins to run from the decided date shown on this page of the decision. The time period does not run from the Mail Date (paper delivery) or Notification Date (electronic delivery).

The subject matter on appeal is directed to a double stranded ("ds") siRNA molecule that down regulates expression of an IKK- γ gene and which has been modified with at least one 2'-O-methyl group and at least one 2'-fluoro group to protect the siRNA from nuclease degradation. Each strand of the siRNA is about 18 to about 28 nucleotides ("nt") in length.

Claims 1, 3, 4, and 7 are illustrative and read (App. Br.³ 25-26):

1. A chemically modified double stranded siRNA molecule that down regulates expression of an IKK-gamma gene via RNA interference (RNAi), wherein: a) each strand of said siRNA molecule is independently about 18 to about 28 nucleotides in length; b) one strand of said siRNA molecule comprises nucleotide sequence having sufficient complementarity to an RNA of said IKK-gamma gene for the siRNA to direct cleavage of said RNA via RNA interference; and (c) wherein said siRNA molecule comprises 2'-O-methyl and 2'-fluoro modifications.

3. The siRNA molecule of claim 1, wherein said siRNA molecule is assembled from two separate oligonucleotide fragments wherein a first fragment comprises the sense strand and a second fragment comprises the antisense strand of said siRNA molecule.

4. The siRNA molecule of claim 3, wherein said sense strand is connected to the antisense strand via a linker molecule.

² Appellant cancelled claim 13 in its Reply Brief under 37 C.F.R. § 41.41 filed 5 September 2008 ("Reply Br."), as acknowledged by the Examiner in a miscellaneous communication mailed 17 September 2008.

³ Supplemental Brief on Appeal filed 13 June 2008 ("App. Br.").

7. The siRNA molecule of claim 3, wherein said second fragment comprises a terminal cap moiety at a 5'-end, a 3'-end, or both of the 5' and 3' ends of said second strand.

The Examiner has rejected

- (A) claims 1-3, 14, and 16 under 35 U.S.C. § 103(a) as unpatentable over Tuschl I⁴ and Tuschl II⁵ in view of Yamaoka,⁶ Smahi,⁷ and Krappmann⁸ (Ans.⁹ 5-8);
- (B) claims 4-6 under 35 U.S.C. § 103(a) as unpatentable over Tuschl I, Tuschl II, Yamaoka, Smahi, and Krappmann taken further in view of Agrawal¹⁰ (Ans. 8);

⁴Published Patent Application US 2002/0086356 A1, *RNA Sequence-Specific Mediators of RNA Interference*, published 4 July 2002, based on application 09/821,832, filed 30 March 2001, by Tuschl et al. ("Tuschl I").

⁵International Publication WO 02/44321 A2, *RNA Interference Mediating RNA Small RNA Molecules*, published 6 June 2002, based on international application PCT/EP01/13968, filed 29 November 2001, by Tuschl et al., which claims priority benefit of US provisional application 60/279,661, filed 30 March 2001 ("Tuschl II").

⁶Yamaoka et al., "Complementation Cloning of NEMO, a Component of the IκB Kinase Complex Essential for NK-κB Activation," *Cell*, 93 (26 June 1998): 1231-1240 ("Yamaoka").

⁷Smahi et al., "Genomic Rearrangement in *NEMO* impairs NF-κB activation and is the cause of incontinentia pigmenti," *Nature*, 405 (25 May 2000):466-472 ("Smahi").

⁸Krappmann et al., "The IκB Kinase (IKK) Complex is Tripartite and Contains IKKγ but not IKAP as a Regular Component," *The Journal of Biological Chemistry*, 275 (22 September 2000):29779-29787 ("Krappmann").

⁹Examiner's Answer mailed 7 July 2008 ("Ans.").

¹⁰International Publication WO 94/01550, *Self-Stabilized Oligonucleotides as Therapeutic Agents*, published 20 January 1994, based on international

- (C) claims 7 and 8 under 35 U.S.C. § 103(a) as unpatentable over Tuschl I, Tuschl II, Yamaoka, Smahi, and Krappmann taken further in view of Matulic-Adamic¹¹ (Ans. 9);
- (D) claims 1-3 under 35 U.S.C. § 103(a) as unpatentable over Kenrick¹² in view of Tuschl I and Tuschl II (Ans. 9-11);
- (E) claims 1-3 and 14-16 under 35 U.S.C. § 103(a) as unpatentable over Elbashir,¹³ Tuschl II, and Bass¹⁴ in view of Yamaoka, Krappmann, and Smahi (Ans. 11-14);
- (F) claims 4-6 under 35 U.S.C. § 103(a) as unpatentable over Elbashir, Tuschl II, Bass, Yamaoka, Krappmann, and Smahi further in view of Agrawal (Ans. 14-15);
- (G) claims 7-8 under 35 U.S.C. § 103(a) as unpatentable over Elbashir, Tuschl II, Bass, Yamaoka, Krappmann, and Smahi further in view of Matulic-Adamic (Ans. 15);

application PCT/US93/06326, filed 2 July 1993, by Agrawal et al. ("Agrawal").

¹¹ US Patent 5,988,203, *Enzymatic Nucleic Acids Containing 5'- and/or 3'Cap Structures*, issued 7 December 1999, to Matulic-Adamic et al. ("Matulic-Adamic").

¹² US Patent 6,824,972 B2, *Diagnosis and Treatment of Medical Conditions Associated with Defective NF κ B (NF- κ B) Activation*, issued 30 November 2004, based on application 09/863,049, filed 22 May 2001, to the Kenrick et al. ("Kenrick").

¹³ Elbashir et al., "Duplexes of 21-nucleotide RNAs mediate RNA interference in cultured mammalian cells," *Nature*, 411 (24 May 2001):494-498 ("Elbashir").

¹⁴ B. Bass, "The short answer," *Nature*, 411 (24 May 2001):428-429 ("Bass").

- (H) claims 1-3, 9, and 14-16 under 35 U.S.C. § 103(a) as unpatentable over Fire¹⁵ and Tuschl II in view of Yamaoka, Krappmann, and Smahi (Ans. 16-18);
- (I) claims 4-6 under 35 U.S.C. § 103(a) as unpatentable over Fire, Tuschl II, Yamaoka, Krappmann, and Smahi further in view of Agrawal (Ans. 18-19); and,
- (J) claims 7-8 under 35 U.S.C. § 103(a) as unpatentable over Fire, Tuschl II, Yamaoka, Krappmann, and Smahi further in view of Matulic-Adamic (Ans. 19-20).¹⁶

The rejections fall into two groups. In the first group, the Examiner relies on (a) Tuschl I, Elbashir, or Fire as teaching sequence-specific inhibition of gene expression by dsRNA (RNA interference or "RNAi"), specifically by siRNA, (b) Tuschl II as teaching 19-21 nucleotide siRNA wherein the 2' OH group of a ribose is replaced by an OR, wherein R is C₁₋₆ alkyl, or a fluoro to improve stability, (c) Yamaoka as teaching the cDNA sequence of an IKK- γ gene, and (d) Krappmann and Smahi each as teaching the relationship between the IKK- κ gene and NF- κ B activation. The Examiner further relies on Agrawal and Matulic-Adamic as teaching additional methods of improving the stability of RNA strands from degradation by nucleases. In the second group, the Examiner relies on Kenrick as teaching methods of treating NF- κ B related medical conditions

¹⁵ US Patent 6,506,559 B1, *Genetic Inhibition by Double-Stranded RNA*, issued 14 July 2003, based on application 09/215,257, to Fire et al. ("Fire").

¹⁶ The Examiner withdrew the rejection of claims 1-9 and 13-16 under 35 U.S.C. §§ 112, first paragraph (written description), and 305 (enlarging the scope of the claimed invention) (Ans. 2-3). Cancellation of claim 13 renders its rejections under 35 U.S.C. § 103(a) moot.

with sequences 100% complementary to an IKK- γ gene and Tuschl I and II as teaching the use of modified siRNA to block mRNA translation *in vivo*.

Appellant argues that the Examiner has failed to give any reason for providing 2'-O-methyl and 2'-fluoro modifications on the same siRNA, especially since Tuschl II is alleged to teach avoiding 2'-O-methyl modifications of the siRNA. Appellant further argues that Yamaoka fails to disclose the cDNA sequence encoding an IKK- γ gene and that the Examiner has failed to provide any reason for down regulating IKK- γ gene expression. Appellant finally argues that the teachings of Agrawal and Matulic-Adamic are directed to antisense and ribozyme interference RNA technology, respectively, and therefore are irrelevant to siRNA interference technology.

At issue is whether Appellant has shown the Examiner reversibly erred in (i) finding that Yamaoka disclosed the cDNA sequence of an IKK- γ gene, (ii) concluding that an ordinarily skilled artisan would have had both a motivation to and a reasonable expectation of success of providing an siRNA molecule with at least one 2'-O-methyl group and at least one 2'-fluoro group, (iii) failing to provide a reason for down regulating an IKK- γ gene, (iv) concluding that it would have been obvious to join a sense and an anti-sense RNA strand into a single ds siRNA via a linker molecule based on the teachings of Agrawal, (v) concluding that it would have been obvious to cap either or both ends of the antisense strand based on the teachings of Matulic-Adamic, and (vi) concluding that Kenwick provided a teaching or suggestion of down regulating IKK- γ gene expression.

Since Appellant has provided separate patentability arguments for claim groupings 4-6 and 7-8, we decide this appeal on the basis of claims 1,

4 and 8. 37 C.F.R. § 41.37(c)(1)(vii). We also note that the Evidence Appendix of the principal brief does not cite to or provide any evidence being relied upon by Appellant in this appeal. 37 C.F.R. § 41.37(c)(2)(ix).

II. Findings of Fact ("FF")

The following findings of fact are supported by a preponderance of the evidence of record.

A. RNA interference

- [1] The central dogma of molecular biology comprises three processes: replication (the copying of parental DNA to form daughter DNA molecules with identical nucleotide sequences), transcription (the process by which parts of the genetic message encoded in DNA are precisely copied into RNA), and translation (whereby the genetic message encoded in messenger RNA ("mRNA") is translated, i.e., expressed, into a protein with a particular amino acid sequence) (see e.g., Lehninger¹⁷ 921-922).
- [2] As stated by Bass, "[o]ne way of seeing what a gene does is to block its messenger RNA and note the effects" (Bass abstract).
- [3] Several strategies can be used to achieve gene-specific inhibition, including single strand nucleic acid mediated antisense¹⁸ technology and dsRNA mediated RNA interference (Fire 1: 63-67; 4:20-28).
- [4] RNA interference ("RNAi") is a cellular process by which a dsRNA sequence-specifically blocks the expression of a gene (Fire 1:17-19;

¹⁷ Lehninger PRINCIPLES OF BIOCHEMISTRY, fourth edition, W.H. Freeman and Company, New York (2005) ("Lehninger") (copy enclosed).

¹⁸ Antisense technology involves a single stranded antisense oligonucleotide pairing with its complementary mRNA to block translation (Fire 1:63-2:20).

Tuschl I ¶3; Bass 428, col. 1, ¶2; Elbashir 494 abstract; Tuschl II 1:11-26).

- [5] According to Fire "dsRNA is at least 100-fold more effective than ... antisense RNA in reducing gene expression" (Fire 3:30-32).
- [6] Similarly, according to Tuschl I and Elbashir, "siRNAs are effective at concentrations that are several orders of magnitude below the concentrations applied in conventional antisense or ribozyme gene targeting experiments" (Tuschl I ¶148; Elbashir p. 496, col. 1, ¶2).
- [7] According to Fire, the dsRNA (i) may be formed by a single self-complementary RNA strand or two complementary RNA strands (i.e., sense and antisense strands), (ii) preferably contains a nucleotide sequence greater than 90% identical to a portion of the gene being targeted for inhibition, (iii) may include modifications to the phosphate-sugar backbone or the nucleoside, and (iv) is at least 25 base pairs long (Fire 4:41-46; 7:31-32, 42-44, 53-54, 64-67; 26:55-59 (claim 10)).
- [8] According to Fire, the dsRNA may be used to inhibit expression of a gene associated with disease causation or symptoms or to identify gene function in an organism (Fire 9:65-10:7; 10:26-28; 12:17-20).
- [9] According to Tuschl I,

RNAi is envisioned to begin with cleavage of the dsRNA to 21-23 nt products by a dsRNA-specific nuclease ... These short dsRNAs might then be dissociated with an ATP-dependent helicase ... to 21-23 nt asRNAs [i.e., antisense RNAs] that could then target the mRNA for cleavage. The short asRNAs are imagined to remain associated with the RNAi-specific proteins ... originally bound by

the full-length dsRNA ... Finally, a nuclease ...
would cleave the mRNA. [Tuschl I ¶36.]

- [10] Thus, Tuschl I is directed 21-23 nt dsRNA molecules useful as sequence-specific mediators of RNAi to inhibit mRNAs that encode proteins associated with or causative of a disease or an undesirable condition (Tuschl I ¶57).
- [11] In other words, according to Tuschl I, if the sequence of the gene to be targeted is known, any dsRNA can be used to mediate RNAi provided that it has sufficient homology to the targeted gene (Tuschl I ¶¶ 57, 59).
- [12] Tuschl I also showed that 21 nt siRNA duplexes were able to specifically inhibit a target gene expression without activating an interferon response (Tuschl I ¶144).
- [13] A preferred embodiment of Tuschl I comprises 21 nt strands with 2 nt overhangs at both 3' ends of the RNA, wherein the 3' overhangs can be modified, e.g., by 2' (deoxy) thymidine substitution, to enhance the stability of the siRNA (Tuschl I ¶¶55, 148).
- [14] According to Tuschl I, the absence of a 2' OH group enhances the nuclease resistance of the 3' overhang *in vitro* (Tuschl I ¶55).
- [15] Elbashir showed that 21 and 22 nt siRNA duplexes mediated sequence-specific mRNA degradation, without activating the interferon system as do dsRNAs having more than 30 base paired nucleotides (Elbashir abstract; p. 495, col. 1, ¶2; p. 496, col. 1, ¶3).
- [16] Specifically, Elbashir synthesized 21-nt siRNA duplexes comprising sense and antisense strands with 2-nt 3' overhangs comprising 2' (deoxy) thymidine because the thymidine overhang reduces the cost

of RNA synthesis and may enhance the nuclease resistance of the siRNA (¶ bridging pp. 495-496; Figure 1).¹⁹

- [17] According to Bass, although RNAi is routine in laboratories to study a wide range of organisms, Tuschl (explicitly referring to Elbashir) describes research that paves the way for successful RNAi use in mammalian cells, namely that siRNAs shorter than about 30 bps mediate a sequence-specific response whereas longer dsRNAs mediate a global, nonspecific response (Bass, p. 428; Figure 1).

B. RNA strand modifications

- [18] Tuschl II discloses 19-25 nt siRNA duplexes capable of mediating RNAi and/or DNA methylation, wherein the most effective dsRNAs comprise two 21 nt strands which base paired such that 1-3, especially 2 nt 3' overhangs are present on both ends of the dsRNA (Tuschl II 3:18-24; 4:18-21).

- [19] According to Tuschl II,

[t]he target RNA cleavage reaction guided by siRNAs is highly sequence-specific. However, not all positions of a siRNA contribute equally to target recognition. Mismatches in the center of the siRNA duplex are most critical and essentially abolish target RNA cleavage. In contrast, the 3' nucleotide of the siRNA strand (e.g., position 21) that is complementary to the single-stranded target

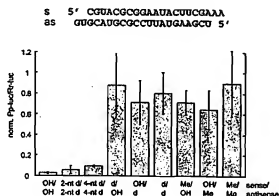
¹⁹ DNA and RNA differ in three main ways. First, RNA is usually a single-stranded molecule in most of its biological roles, whereas DNA is usually double-stranded. Second, RNA contains a ribose sugar, whereas DNA contains a deoxyribose sugar (i.e., deoxyribose does not have an OH group attached to the 2' position of the sugar ring). Third, the complementary base to adenine in RNA is uracil, not thymine as it is in DNA.

RNA, does not contribute to specificity of the target recognition. Further, the sequence of the unpaired 2-nt 3' overhang of the siRNA strand with the same polarity as the target RNA is not critical for target RNA cleavage as only the antisense siRNA strand guides target recognition. Thus, from the single-stranded overhanging nucleotides only the penultimate position of the antisense siRNA (e.g., position 20) needs to match the targeted sense mRNA. [Tuschl II 4:23-5:2.]

- [20] In other words, according to Tuschl II, the cleavage sites for both sense and antisense target RNAs are located in the middle of the region spanned by the siRNA duplexes (Tuschl II 47:4-5).
- [21] Tuschl II discloses stabilizing the 3' overhangs against degradation to enhance *in vivo* and *in vitro* stability of the siRNAs (Tuschl II 5:4-9).
- [22] According to Tuschl II, absence of a 2' OH group enhances the nuclease resistance of the overhang *in vitro* (Tuschl II 5:11-13).
- [23] For example, Tuschl II discloses that "[i]n preferred sugar-modified ribonucleotides the 2' OH-group is replaced by a group selected from H, OR, R, halo, SH, SR, NH₂, NHR, NR₂ or CN, wherein R is C₁-C₆ alkyl, alkenyl or alkynyl and halo is F, Cl, Br or I" (Tuschl II 5:31-6:2) as well as replacing uridine residues with 2' deoxy thymidine (*id.* 21:1-2; 40:19-29).
- [24] Referring to Figure 14, Tuschl II states that substitution of the 2-nt 3' overhangs by 2'-deoxy nucleotides (d) had no effect on RNAi activity and replacement of two additional ribonucleotides adjacent to the overhangs in the paired region left significant RNAi activity. However, complete substitution of one or both siRNA strands by 2'-

deoxy residues or by 2'-O-methyl residues abolished RNAi. (Tuschl II 46:5-14).

- [25] Figure 4 of Tuschl II depicts the effect of substituting the 2'-hydroxyl groups of the siRNA ribose residues. The 2'-hydroxyl groups (OH) in the strands of siRNA duplexes were replaced by 2'-deoxy (d) or 2'-O-methyl (Me). 2-nt and 4-nt 2'-deoxy substitutions at the 3'-ends are indicated as 2-nt d and 4-nt d, respectively. Uracine residues were replaced by 2'-deoxy thymidine. [Tuschl II 20:28-21:2.] Figure 4 is reproduced below.



{Figure 14 of Tuschl II depicts the effect of substituting the 2'-OH groups of siRNA ribose residues.}

- [26] Agrawal discloses antisense oligonucleotides that have increased resistance to nucleases, noting that even nuclease resistant 3' capped oligonucleotides can become degraded eventually as their 3' capped end is slowly digested by a combination of endonuclease and exonuclease activities (Agrawal 1:8-9; 3:4-26).
- [27] In a preferred embodiment, Agrawal discloses oligonucleotides comprising a target hybridizing region and a self-complementary

region, wherein the self-complementary region is connected to the target hybridizing region by a non-nucleic acid linker, e.g., an (ethylene glycol)₁₋₆ linker (Agrawal 8:22-24; 15:31-36).

[28] Agrawal further discloses an embodiment wherein the oligonucleotide is hyperstabilized by incorporating one or more 2'-O-Me ribonucleotides into the self-complementary region and using DNA within the complementary portion of the target hybridizing region or vice versa because DNA:RNA interactions are more stable than DNA:DNA interactions (Agrawal 16:24-35).

[29] Matulic-Adamic discloses incorporating chemical modifications at the 5' and/or 3' ends of ribozymes, i.e., RNAs which can enzymatically cleave other RNA molecules in a nucleotide base specific manner, to protect the ends from exonuclease degradation (Matulic-Adamic 1:14-17; 2:44-54).

C. IKK- γ : its sequence and relationship to NF- κ B activation

[30] IKK- γ is also known as NEMO (NF- κ B Essential Modulator) (828 patent specification 8:31-32; Kenwrick 2:39-42; Krappmann abstract).

[31] NF- κ B plays a pivotal role in many cellular processes, including inflammation, the immune response, cell proliferation, and apoptosis (Krappmann 29779 ¶1).

[32] According to Krappmann, specific down regulation of IKK- γ protein levels by antisense oligonucleotides significantly reduced cytokine mediated activation of the IKK complex and subsequent NF- κ B activation (Krappmann abstract; 29780, col. 2, ¶2).

- [33] Kenwick also discloses that the absence of IKK- γ protein results in a complete inhibition of NF- κ B activation (Kenwick 2:42-46).
- [34] Yamaoka cloned a 48 kDa murine IKK- γ /NEMO protein and also found that it was essential for NF- κ B activation (Yamaoka abstract; 1233-1234 "Molecular Cloning of NEMO;" 1238, col. 2, ¶2).
- [35] Yamaoka deposited the NEMO cDNA sequence with GenBank under accession number AF069542 and provided the amino acid sequence of the protein in Figure 3 (Yamaoka 1234, 1240).
- [36] We find that it is well within ordinary skill in the art to access the publicly available gene sequence database GenBank (<http://www.ncbi.nlm.nih.gov/Genbank/index.html>) to obtain the NEMO cDNA sequence reported by Yamaoka under accession number AF069542.
- [37] Smahi discloses that most cases of familial incontinentia pigmenta (IP), a genodermatosis that is usually lethal prenatally in males and that causes abnormalities of the skin, hair, nails, teeth, eyes, central nervous system in affected females, are caused by mutations in the NEMO/IKK- γ gene (Smahi abstract).
- [38] Kenwick discloses a method treating NF- κ B related medical conditions, such as IP, by administering therapeutically effective amounts of IKK- γ /NEMO nucleic acid of SEQ ID NO:1, a 23106 nt DNA (Kenwick 4:24-28, 42-43; 49: <210> - <213>).
- [39] Kenwick also discloses approximately sixty-seven sequences, generally about 20 nt in length, for use as primers and probes in

assays and kits for detecting mutations of SEQ ID NO:1 in an organism (Kenrick 5:33-7:29; SEQUENCE LISTING, cols. 73-90).

III. Discussion

As noted above, the pending rejections fall into two groups. While the primary references (i.e., Tuschl I, Ebashir (alone or in combination with Bass), or Fire) in each rejection of the first group are different, each rejection relies on common secondary (i.e., Tuschl II, Yamaoka, Krappmann, and Smahi) and tertiary (i.e., Agrawal and Matulic-Adamic) references, thereby raising common issues. Consequently, these rejections are addressed together.

A. The first group of rejections

1. Findings and conclusions of the Examiner

a. claim 1

As to claim 1, the Examiner found that Tuschl I teaches using 21-23 nt dsRNA molecules with 2'-deoxy modifications to mediate RNAi, if the sequence of the gene to be targeted is known, because siRNAs are effective at concentrations several orders of magnitude below concentrations used in conventional antisense or ribosome gene targeting experiments (Ans. 6). The Examiner found that Tuschl I differs in failing to disclose siRNA molecules having both 2'-O-methyl and 2'-fluoro modifications (Ans. 6) and that down regulate the IKK- γ gene (Ans. 7).

The Examiner found that Elbashir teaches that 21 nt siRNAs with 2 nt 3' overhangs and 2'-thymidine modifications mediate RNAi at concentrations several orders of magnitude lower than concentrations used in conventional antisense or ribosome gene targeting experiments (Ans. 12).

The Examiner found that Bass teaches that once the sequence of gene is known, RNAi may be used to determine its function, that RNAi is a routine technology, and that siRNA mediated RNAi triggers degradation of mRNA at concentrations several orders of magnitude lower than concentrations used in conventional antisense or ribosome gene targeting experiments (Ans. 13). The Examiner found that Elbashir differs in failing to disclose siRNA molecules having both 2'-O-methyl and 2'-fluoro modifications (Ans. 12) and that neither Elbashir nor Bass disclose siRNAs that down regulate the IKK- γ gene (Ans. 13).

The Examiner found that Fire discloses dsRNA mediated inhibition of gene expression, wherein the dsRNA comprised (i) at least 25 base pairs, (ii) complementary sense and antisense strands, the antisense strand being at least 90% complementary to the nucleotide sequence of a target gene, and (iii) optionally, one or more modifications to either the phosphate-sugar backbone or nucleoside (Ans. 16). The Examiner found that Fire discloses that dsRNA mediated RNAi is at least 100-fold more effective than an equivalent concentration of antisense RNA in reducing gene expression (Ans. 17). The Examiner found that Fire differs in failing to disclose siRNA molecules having both 2'-O-methyl and 2'-fluoro modifications and that down regulate the IKK- γ gene (Ans. 17).

The Examiner found that Tuschl II teaches 19-25 nt dsRNAs with 3' end overhangs which act as guide RNAs for sequence specific mRNA degradation and show high stability *in vivo* or *in vitro* (Ans. 6, 12, 1). The Examiner also found that Tuschl II teaches substituting 2' OR (wherein R is

C₁₋₆ alkyl) and/or fluoro groups for the 2' OH groups of the RNA sugars (Ans. 6-7, 13, 17).

The Examiner found that Yamaoka discloses the cDNA sequence encoding a 48 kDa IKK- γ protein (Ans. 7, 13, 17).

The Examiner found that Krappmann discloses that specific down regulation of IKK- γ protein levels by antisense oligonucleotide significantly reduced cytokine mediated activation of IKK complex and subsequent NF- κ B activation (Ans. 7, 13, 18).

The Examiner found that Smahi identifies the IKK- γ gene as target for experimental gene silencing because mutations in this gene are associated with the genetic disease IP (Ans. 7, 14, 18).

The Examiner found that the level of skill in the art is high (Ans. 8, 14, 18).

The Examiner concluded that it would have been obvious to combine the teachings of Tuschl I or Elbashir or Fire with the teachings of Tuschl II to produce chemically modified, stable ds siRNA (Ans. 7, 13, 17). The Examiner further concluded that it would have been obvious to combine the teachings of Tuschl I or Elabshir or Fire with the teachings of Tuschl II and with the teachings of Smahi, Krappmann, and Yamaoka to produce siRNA molecules that down regulate the IKK- γ gene because Krappmann discloses antisense mediated down regulation of the IKK- γ gene, Smahi teaches that the IKK- γ gene is a desirable target, and Tuschl I, Elbashir, and Fire each teach that siRNAs are more powerful than conventional antisense or ribozyme mediated gene targeting experiments (Ans. 7-8, 14, 18). The Examiner concluded that one of ordinary skill in the art would have had a

reasonable expectation of success of producing chemically modified siRNA molecules that down regulate the IKK- γ given the teachings of the applied references and the high level of skill in the art.

b. claim 4

As to claim 4, the Examiner found that none of Tuschl I, Elbashir, Bass, Fire, Tuschl II, Smahi, Krappmann or Yamaoka discloses connecting the sense and antisense strands of the siRNA by a linker (Ans. 8, 14, 18).

The Examiner found that Agrawal discloses antisense oligonucleotides with increased resistance to degradation by nucleases, including both exo- and endo-nucleases; and, which formed stable hybrids with target sequences and activated RNase H (i.e., mediated RNAi) (Ans. 8, 14, 19). The Examiner found that the antisense oligonucleotide of Agrawal contained (i) a self-complementary region which self-paired, resulting in formation of a hairpin loop containing a polynucleotide linker; and, (ii) a target hybridization region which may be connected to the self-complementary region via a non-nucleic acid linker (Ans. 8, 15, 19).

The Examiner concluded that it would have been obvious to combine the teachings of Agrawal with the teachings of the references applied against claim 1 because Agrawal suggests forming stable, nuclease-resistant duplexes using linkers capable of mediating RNAi (Ans. 8, 15, 19).

c. claim 7

As to claim 7, the Examiner found that none of Tuschl I, Elbashir, Bass, Fire, Tuschl II, Smahi, Krappmann or Yamaoka discloses fragments [sic, overhangs?] comprising terminal caps (Ans. 9, 15, 19).

The Examiner found that Matulic-Adamic discloses chemically capping the 5' and/or 3' ends of ribozymes, i.e., nucleic acids that are particularly use for enzymatic cleavage of RNA, to protect the ribozyme from exonuclease degradation (Ans. 9, 15, 19).

The Examiner concluded that it would have been obvious to combine the teachings of Matulic-Adamic with the teachings of the references applied against claim 1, i.e., to end cap the siRNA, because Matulic-Adamic teaches that end capping protects against exonuclease degradation (Ans. 9, 15, 19-20).

2. Appellant's arguments

Initially, we note that arguments based on evidence which has not been cited as relied upon in the Evidence Appendix of the principal brief or provided therewith have not been considered. 37 C.F.R. § 41.37(c)(2)(ix).

a. claim 1

In essence, Appellant argues that there was little, if any, reason for one of ordinary skill in the art to modify siRNAs with both 2'-O-methyl and 2'-deoxy-2'-fluoro modifications because one could not have predicted which modifications might be efficacious and because Tuschl II was said to teach away for the claimed modification (App. Br. 12-13).

Specifically Appellant argues that Tuschl II expressly warns against using more than two 2'-deoxy modified nucleotides at the strands' 3'-ends or using any 2'-O-methyl modifications, i.e.:

2'-deoxy substitutions of the 2-nt 3' overhanging ribonucleotides do not affect RNAi, but help to reduce the costs of RNA synthesis and may enhance RNase resistance of siRNA duplexes. More extensive 2'-deoxy or 2'-O-methyl

modifications, however, reduce the ability of siRNAs to mediate RNAi, probably by interfering with protein association for siRNAP assembly.
[Tuschl II 49:28-50:2.]

(App. Br. 13). Appellant further argues that since Tuschl II fails to state expressly the effect of 2'-O-methyl substitution on page 46, Tuschl II can only be read teaching the entire avoidance of 2'-O-methyl modifications (App. Br. 13). Thus, Appellant concludes:

[b]ecause 2'-deoxy and 2'-O-methyl modifications were regarded as beneficial to other nucleic acid inhibitors known in the art at the time, and these modifications are found by Tuschl to be not tolerated at all (in the case of 2'-O-methyl modification), or under very limited circumstances (in the case of 2'-deoxy modification), the art of chemically modifying siRNA molecules was highly unpredictable, and the ... ribozyme and/or antisense art predating the present invention does nothing to alleviate this unpredictability. [App. Br. 14.]

Appellant further argues that since Smahi shows that mutation of the IKK- γ gene result in death or disease, one skilled in the art would not have been motivated to down regulate the IKK- γ gene unless he was interested in causing death or disease (App. Br. 14-15). Appellant points out that Elbashir fails to disclose an siRNA that down regulates IKK- γ gene (App. Br. 19).

Appellant also argues that Yamaoka does not disclose an IKK- γ cDNA sequence (App. Br. 15).

Appellant argues that Bass teaches that RNAi can occur by different pathways, one mediated by long dsRNA (at least 30 nt in length) molecules

and the other by short dsRNA (siRNA) molecules; and, that Bass' reference to RNAi as a routine laboratory procedure refers to the long dsRNA pathway (App. Br. 19, 21). Thus, Appellant reasons, one of ordinary skill in the art would have understood Fire to have mistakenly stated that dsRNA molecules of 25 nt in length were operative because dsRNA molecules smaller than 30 nts were inoperative (App. Br. 21).

b. claim 4

Appellant argues that antisense molecules are substantially single stranded prior to interacting with their target and, thus, more susceptible to nuclease attack than is a double stranded nucleic acid molecule (App. Br. 16). Moreover, when Tuschl II limited applicability of 2'-deoxy modifications and avoidance of 2'-O-methyl modifications are considered, Agrawal does not inform or lend predictability to the art of chemically modified siRNA molecules (App. Br. 16). [See also App. Br. 20, 22.]

c. claim 7

In a similar vein, Appellant argues that ribozymes are substantially single stranded prior to interacting with their target and, thus, more susceptible to nuclease attack than is a double stranded nucleic acid molecule (App. Br. 17). Moreover, when Tuschl II limited applicability of 2'-deoxy modifications and avoidance of 2'-O-methyl modifications are considered, Matulic-Adamic does not inform or lend predictability to the art of chemically modified siRNA molecules (App. Br. 17-18). [See also App. Br. 20, 22.]

3. Legal principles

“Section 103 forbids issuance of a patent when ‘the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains.’” *KSR Int’l Co. v. Teleflex Inc.*, 550 U.S. 398, 406, 127 S. Ct. 1727 (2007). The question of obviousness is resolved on the basis of underlying factual determinations including (1) the scope and content of the prior art, (2) any differences between the claimed subject matter and the prior art, (3) the level of skill in the art, and (4) where in evidence, so-called secondary considerations. *Graham v. John Deere Co.*, 383 U.S. 1, 17-18 (1966). In *KSR*, the Supreme Court reaffirmed principles based on its precedent that “[t]he combination of familiar elements according to known methods is likely to be obvious when it does no more than yield predictable results.” *KSR*, 550 U.S. at 416. The Court emphasized that “rejections on obviousness grounds cannot be sustained by mere conclusory statements; instead, there must be some articulated reasoning with some rational underpinning to support the legal conclusion of obviousness” *id.* at 418 (citing *In re Kahn*, 441 F.3d 977, 988 (Fed. Cir. 2006)). However, “the analysis need not seek out precise teachings directed to the specific subject matter of the challenged claim, for a court can take account of the inferences and creative steps that a person of ordinary skill in the art would employ.” *Id.* Thus, “[i]n considering motivation in an obviousness analysis, we ask ‘whether a person of ordinary skill in the art, possessed with the understandings and knowledge reflected in the prior art,

and motivated by the general problem facing the inventor, would have been led to make the combination recited in the claims." *Optivus Tech., Inc. v. Ion Beam Applications S.A.*, 469 F.3d 978, 990 (Fed. Cir. 2006) (citing *In re Kahn*, 441 F.3d at 988). "Non-obviousness cannot be established by attacking references individually where the rejection is based upon the teachings of a combination of references." *In re Merck & Co., Inc.*, 800 F.2d 1091, 1097 (Fed. Cir. 1986).

4. Analysis

Here, Tuschl I, Elbashir, and Fire each teach dsRNAs about 18 to about 28 nucleotides in length (FF 7, 10, 13, 15, 16) that mediate RNAi (FF 3, 4, 7-8, 9-10, 12, 15) at concentrations several orders of magnitude below the concentrations needed in conventional antisense or ribozyme gene targeting experiments and, thus, suggest the usefulness of these siRNAs in gene targeting experiments (FF 5, 6). Gene targeting may be used to inhibit expression of a gene associated which encodes a protein associated with or causative of disease or other undesirable conditions or to study the function of gene (FF 2, 8). Tuschl II discloses siRNA duplexes 19-25 nucleotides in length that mediate RNAi (FF 19) and a proposed molecular explanation of how siRNA mediated RNAi works (FF 19).

Tuschl I and Tuschl II teach and/or suggest that the most effective siRNA molecules comprise two 21 nt strands which are base paired such that 1-3, especially 2 nt 3' overhangs are present on both ends of the siRNA duplex (FF 13, 18). Thus, each strand of the siRNA is single-stranded in its 3' overhang. According to both Tuschl I and Tuschl II, the absence of a 2'-OH group enhances the nuclease resistance of the 3' overhang (FF 14, 22).

Moreover, Fire, Tuschl I, Elbashir, and Tuschl II each teach the siRNA may include modifications to phosphate-sugar backbone and/or nucleoside (FF 7, 13, 16, 21).

Modifications of nucleic acids to stabilize them against degradation by nucleases was known in the art. Tuschl II preferably substitutes the 2'-OH groups of 3' overhang (i.e., single stranded) portion of siRNAs with OR groups to form C₁₋₆ alkyl ester groups, e.g., methyl esters, and halide groups, e.g., fluoro, as well as replacing uridine residues with 2'-deoxy thymidines, to enhance the nuclease resistance of the overhang portion (FF 23). Similarly, Matulic-Adamic chemically modifies the 5' and/or 3' ends of ribozymes to protect them from exonuclease degradation (FF 29). Agrawal notes that even nuclease resistant 3' capped oligonucleotides can become degraded eventually as their 3' capped end is slowly digested by a combination of endonuclease and exonuclease activity (FF 26) and discloses antisense oligonucleotides wherein regions of the antisense are connected via linkers (FF 27).

Therefore, we agree with the Examiner that it would have been obvious to modify an siRNA, particularly at nucleotides in a 1-3 nt of a 3' overhang at the end of one or both strands, to increase the resistance of siRNA to nuclease degradation using modifications known and used for increasing the stability of RNA to nuclease degradation. We also agree with the Examiner that it would have been obvious to select an IKK- γ as a gene for targeted experimentation because of its known relationship with NF- κ B activation as disclosed by Krappmann (FF 32) and/or its causal relationship

to IP as disclosed by Smahi (37) given Yamaoka's disclosed cDNA and amino acid sequences for an IKK- γ gene (FF 34-36).

Appellant's arguments do not persuade us to the contrary.

Nucleic acid molecules are known to be degraded or hydrolyzed by nucleases *in vivo* and in culture systems and, thus, it is routine in the art to modify nucleic acids to resist nuclease hydrolysis (see e.g., FF 16, 21, 26, 29). Exonucleases by definition hydrolyze nucleic acid molecules from their ends, while endonucleases attack nucleic molecules between their ends. Modifications which interfere with the interaction between a nucleotide substrate and a nuclease enzyme's active site would reasonably be expected to increase a nucleic acid's resistance to nuclease degradation. Thus, it is not unexpected, and in fact is entirely predictable, that a double stranded nucleic acid would be less susceptible to nuclease degradation than a single stranded nucleic acid since one strand would reasonably be expected to block a nuclease's, particularly an endonuclease's, access to the other strand to some degree. Indeed, Appellant even points out that single stranded nucleic acids are more susceptible to nuclease degradation than double stranded nucleic acids (see e.g., App. Br. 16-17). Similarly, capping one or both ends of a nucleic acid molecule, as disclosed by Matulic-Adamic, or forming a double-stranded portion within an antisense molecule, as disclosed by Agrawal, would also reasonably be expected to sterically interfere with the active site of a nuclease. By the same token, the most effective siRNA molecules are disclosed as having 3' overhangs (see e.g., FF 13, 18) and, therefore, would reasonably be expected to be more susceptible to nuclease degradation by virtue of being single stranded structures. Moreover, Tuschl

I and Tuschl II identify a specific site of nuclease attack, i.e., the 2'-OH group of the nucleotide (FF 14, 22). Therefore, it would have been obvious to modify the 2'-OH group of the 3' overhang of siRNAs to increase the nuclease resistance of the siRNA. The combination of chemical modifications known to increase the nuclease resistance of nucleic acid molecules to siRNA molecules, particularly to the 2'-OH group of a single stranded 3' overhang, is likely to be obvious when it does no more than yield a predictable result.

Furthermore, claim 1 only requires the recited siRNA to have a single 2'-O-methyl modification and a single 2'-fluoro modification. For example, if the siRNA had a 3 nt 3' overhang, the end nucleotide might be modified with a 2'-O-methyl group and the middle nucleotide of the overhang might be modified with a 2'-fluoro group. However, overmodification of the 2'-OH groups is expressly warned against by Tuschl II, e.g., complete substitution of the 2'-OH groups of one or both siRNA strands abolishes RNAi (FF 24). Moreover, Tuschl II teaches that the 3' overhang does not contribute to specificity of the target recognition (FF 19), a teaching which have reasonably suggested that chemical modifications to the 3' overhang would be less likely to interfere with the efficacy of the siRNA. Indeed, this appears to be consistent with the data presented in the bar graph of Tuschl II Figure 4 (FF 25). Thus, even assuming *arguendo* that Tuschl II warned against modifying more than two 2'-OH groups at the 3' ends of the siRNA, this argument is not convincing because modifying just two 2'-OH groups at the 3' overhangs (ends) of the siRNA is within the scope of the claimed invention.

Appellant's argument that Tuschl II teaches avoiding any 2'-O-methyl modifications (App. Br. 13) is likewise unpersuasive and misstates Tuschl II. A fair reading of Tuschl II at column 49, line 28, through column 50, line 2, as pointed out by the Examiner (see e.g., Ans. 22), is that more extensive 2'-deoxy or 2'-O-methyl modifications beyond the two nucleotide 3' overhang reduces the ability of siRNAs to mediate RNAi. Moreover, stating that *complete* substitution of one or both siRNA stands by 2'-O-methyl groups abolished RNAi (FF 24), is not synonymous with stating that *any* 2'-O-methyl group modification should be avoided. Therefore, this argument is not persuasive.

Appellant's argument that Smahi fails to provide a motivation for targeting an IKK- γ gene for down regulation by RNAi because down regulated an already defective gene could cause death or disease is unpersuasive for a number of reasons. The Examiner is relying on the combination of Krappmann and Smahi as a reason to study a down regulated IKK- γ gene. As noted by the Examiner (Ans. 25), Krappmann discloses the importance of down regulating an IKK- γ gene, i.e., down regulating IKK- γ reduces subsequent NK- κ B activation, which plays a pivotal response in cellular processes, e.g., inflammation (FF 31-32). Thus, the Examiner essentially concluded that it would have been obvious to down regulate or knock down an IKK- γ gene to study the effect on cellular processes, e.g., inflammation. Smahi discloses that most cases of IP are caused by mutations in the IKK- γ gene (FF 37). The Examiner again found that the IKK- γ gene is a desirable gene for experimental gene silencing (Ans. 7, 14, 18). Thus, the Examiner evidently concluded that it would have been

obvious to experimentally silence an IKK- γ gene to provide a knock-down experimental IP study system. Therefore, Krappmann and/or Smahi suggest studying the IKK- γ gene by experimental silencing. Moreover, the claimed invention is not directed to treating any specific disease or condition by administering a therapeutically effective amount of an IKK- γ gene down regulating siRNA. Therefore, this argument is not persuasive.

Next, Appellant is correct that Yamaoka did not expressly recite the cDNA sequence he obtained. However, Yamaoka expressly stated that the cDNA sequence was deposited with GenBank under accession number AF069542 (FF 35), which is analogous to a deposit of biological material made to satisfy the written description requirement of 35 U.S.C. § 112, first paragraph. It would have been well within ordinary skill in the art, which as the Examiner noted is high, to obtain the deposited cDNA sequence from the publicly available GenBank database (FF36). This is entirely routine and predictable (FF36). Alternatively, Yamaoka expressly disclosed the amino acid sequence of the protein encoded by the cDNA (FF 35), thereby providing a generic description of the DNA sequences encoding the IKK- γ protein. *See e.g., In re Wallach*, 378 F.3d 1330, 1333-34 (Fed. Cir. 2004) (an amino acid sequence supports the entire genus of DNA sequences that can encode the amino acid sequence because the state of the art has developed such that it is routine matter to convert one to the other). Therefore, Appellant's argument that Yamaoka did not disclose an IKK- γ cDNA sequence is not well taken.

Finally, Appellant's argument that one of ordinary skill in the art would interpret Fire as inoperative for dsRNAs of 25 nucleotides in length is

not persuasive. A patent is presumed valid. 35 U.S.C. § 282. In addition, claim 10 of Fire expressly recites a method of RNAi wherein the dsRNA is at least 25 bases in length (FF 7). "The burden of establishing invalidity of a patent or any claim thereof shall rest on the party asserting such invalidity." 35 U.S.C. § 282. Appellant's conclusory statement that one of ordinary skill in the art would have understood Fire to be mistaken in its specification and claims is insufficient to meet this burden. *In re Schulze*, 346 F.2d 600, 602 (CCPA 1965) (argument in the brief does not take the place of evidence of record).

Based on the foregoing, we sustain the rejections of claims 1-3, 14, and 16 under § 103 over the combined teachings of Tuschl I, Tuschl II, Yamaoka, Smahi, and Krappmann; claims 4-6 under § 103 over the combined teachings of Tuschl I, Tuschl II, Yamaoka, Smahi, Krappmann, and Agrawal; claims 7 and 8 under § 103 over the combined teachings of Tuschl I, Tuschl II, Yamaoka, Smahi, Krappmann, and Matulic-Adamic;

claims 1-3 and 14-16 under § 103 over the combined teachings of Elbashir, Tuschl II, Bass, Yamaoka, Krappmann, and Smahi; claims 4-6 under § 103 over the combined teachings of Elbashir, Tuschl II, Bass, Yamaoka, Krappmann, Smahi, and Agrawal; claims 7-8 under § 103 over the combined teachings of Elbashir, Tuschl II, Bass, Yamaoka, Krappmann, Smahi, and Matulic-Adamic;

claims 1-3, 9, and 14-16 under § 103 over the combined teachings of Fire, Tuschl II, Yamaoka, Krappmann, and Smahi; (I) claims 4-6 under § 103 over the combined teachings of Fire, Tuschl II, Yamaoka, Krappmann,

Smahi, and Agrawal; and, claims 7-8 under § 103 over the combined teachings of Fire, Tuschl II, Yamaoka, Krappmann, Smahi, and Matulic-Adamic.

B. The second group of rejections

The second group of rejections only contains a single rejection, i.e., claims 1-3 are rejected under § 103 over the combined teachings of Kenrick, Tuschl I, and Tuschl II.

1. Findings and conclusions of the Examiner

The Examiner found that Kenrick teaches methods of treating NK-κB related medical conditions by administering therapeutically effective amounts of SEQ ID NO:1 (Ans. 10, 32). Kenrick SEQ ID NO:1 is a 23106 nt IKK-γ DNA sequence (FF 38). The Examiner also found that Kenrick discloses "a large number of short nucleic acids," five of which are 100% complementary to an IKK-γ mRNA (SEQ ID NOs:49, 50, 54, 56, and 61) (Ans. 10). The Examiner found that Kenrick differs in failing to disclose siRNA molecules comprising 2'-O-methyl and 2'-fluoro group modifications, wherein the siRNA molecules also down regulate expression of the IKK-γ gene (Ans. 10).

The Examiner concluded that it would have been obvious to produce double stranded siRNA molecules that down regulate IKK-γ gene expression since Kenrick teaches IKK-γ gene sequences and Tusch I and Tuschl II teach methods of producing chemically modified double stranded siRNA molecules (Ans. 10-11, 32-33).

2. Appellant's arguments

Appellant argues that Kenrick teaches DNA fragments which are used as primers to amplify and detect IKK- γ nucleic acids and that Kenrick does not teach down regulation of IKK- γ gene expression for any reason. In essence, Appellant argues the rejection of claims 1-3 over Kenrick, Tuschl I, and Tuschl II is a classic hindsight reconstruction of the claimed invention.

3. Legal principles

"One cannot use hindsight reconstruction to pick and choose among isolated disclosures in the prior art to deprecate the claimed invention." *In re Fine*, 837 F.2d 1071, 1075 (Fed. Cir. 1988).

4. Analysis

Here, we agree with Appellant. Kenrick discloses a method of treating NK- κ B related medical conditions by administering therapeutically effective amounts of the IKK- γ gene, i.e., SEQ ID NO:1 (FF 38). Implicitly, Kenrick is seeking to correct an abnormal IKK- γ gene. This interpretation is consistent with Kenrick's disclosure of well over sixty short DNA sequences as primers and probes in assays and kits for detecting mutations in SEQ ID NO:1, i.e., the IKK- γ gene (FF 39). The Examiner has failed to explain why Kenrick would have suggested down-regulating a gene that he is trying to repair, i.e., replace with SEQ ID NO:1. Rather, it appears that the Examiner has fallen into the trap of hindsight reconstruction.

Based on the foregoing, we reverse the rejection of claims 1-3 under § 103 over the combined teachings of Kenrick, Tuschl I, and Tuschl II.

D. Conclusion

Appellant has failed to show the Examiner reversibly erred in (i) finding that Yamaoka disclosed the cDNA sequence of an IKK- γ gene, (ii) concluding that an ordinarily skilled artisan would have had both a motivation to and a reasonable expectation of success of providing an siRNA molecule with at least one 2'-O-methyl group and at least one 2'-fluoro group, (iii) failing to provide a reason for down regulating an IKK- γ gene, (iv) concluding that it would have been obvious to join a sense and an anti-sense RNA strand into a single ds siRNA via a linker molecule based on the teachings of Agrawal, or (v) concluding that it would have been obvious to cap either or both ends of the antisense strand based on the teachings of Matulic-Adamic. However, Appellant has shown that the Examiner reversibly erred in (vi) concluding that Kenwrick provided a teaching or suggestion of down regulating IKK- γ gene expression.

IV. Order

Upon consideration of the record, and for the reasons given, it is

ORDERED that the decision of the Examiner to reject claims 1-3, 14, and 16 under 35 U.S.C. § 103(a) as unpatentable over Tuschl I and Tuschl II in view of Yamaoka, Smahi, and Krappmann is AFFIRMED;

FURTHER ORDERED that the decision of the Examiner to reject claims 4-6 under 35 U.S.C. § 103(a) as unpatentable over Tuschl I, Tuschl II, Yamaoka, Smahi, and Krappmann taken further in view of Agrawal is AFFIRMED;

FURTHER ORDERED that the decision of the Examiner to reject claims 7 and 8 under 35 U.S.C. § 103(a) as unpatentable over Tuschl I,

Tuschl II, Yamaoka, Smahi, and Krappmann taken further in view of Matulic-Adamic is AFFIRMED;

FURTHER ORDERED that the decision of the Examiner to reject claims 1-3 under 35 U.S.C. § 103(a) as unpatentable over Kenrick in view of Tuschl I and Tuschl II is REVERSED;

FURTHER ORDERED that the decision of the Examiner to reject claims 1-3 and 14-16 under 35 U.S.C. § 103(a) as unpatentable over Elbashir, Tuschl II, and Bass in view of Yamaoka, Krappmann, and Smahi is AFFIRMED;

FURTHER ORDERED that the decision of the Examiner to reject claims 4-6 under 35 U.S.C. § 103(a) as unpatentable over Elbashir, Tuschl II, Bass, Yamaoka, Krappmann, and Smahi further in view of Agrawal is AFFIRMED;

FURTHER ORDERED that the decision of the Examiner to reject claims 7-8 under 35 U.S.C. § 103(a) as unpatentable over Elbashir, Tuschl II, Bass, Yamaoka, Krappmann, and Smahi further in view of Matulic-Adamic is AFFIRMED;

FURTHER ORDERED that the decision of the Examiner to reject claims 1-3, 9, and 14-16 under 35 U.S.C. § 103(a) as unpatentable over Fire and Tuschl II in view of Yamaoka, Krappmann, and Smahi is AFFIRMED;

FURTHER ORDERED that the decision of the Examiner to reject claims 4-6 under 35 U.S.C. § 103(a) as unpatentable over Fire, Tuschl II, Yamaoka, Krappmann, and Smahi further in view of Agrawal is AFFIRMED;

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FURTHER ORDERED that the decision of the Examiner to reject claims 7-8 under 35 U.S.C. § 103(a) as unpatentable over Fire, Tuschl II, Yamaoka, Krappmann, and Smahi further in view of Matulic-Adamic is AFFIRMED; and,

FURTHER ORDERED that requests for extending time for taking any subsequent action in connection with this appeal are governed by 37 C.F.R. § 1.550(c).

AFFIRMED

Ack

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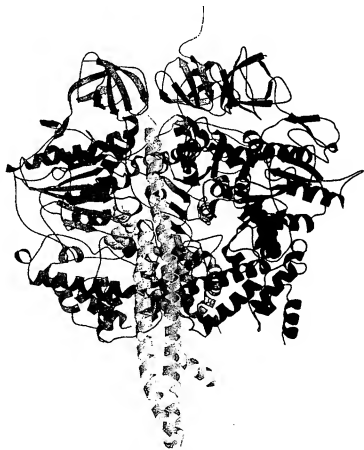
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INFORMATION PATHWAYS

Genes and Chromosomes	923
DNA Metabolism	948
RNA Metabolism	995
Protein Metabolism	1034
Regulation of Gene Expression	1081

The third and final part of this book explores the biochemical mechanisms underlying the apparently contradictory requirements for both genetic continuity and evolution of living organisms. What is the molecular nature of genetic material? How is genetic information transmitted from one generation to the next with high fidelity? How do the rare changes in genetic material arise? How are the raw material of evolution expressed in the amino acid sequences of the astonishing variety of protein molecules in a living cell?

The fundamental unit of information in living systems is the **gene**. A gene can be defined biochemically as a segment of DNA (or, in a few cases, RNA) that encodes the information required to produce a functional biological product. The final product is usually a protein, so much of the material in Part III concerns genes that encode proteins. A functional gene product might be one of several classes of RNA molecules. The storage, maintenance, and metabolism of these informational units form the focal points of our discussion in Part III.

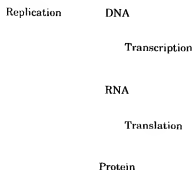
Modern biochemical research on gene structure and function has brought to biology a revolution comparable to that stimulated by the publication of Darwin's theory on the origin of species nearly 150 years ago. An understanding of how information is stored and used in

cells has brought penetrating new insights to some of the most fundamental questions about cellular structure and function. A comprehensive conceptual framework for biochemistry is now unfolding.

Today's understanding of information pathways has arisen from the convergence of genetics, physics, and chemistry in modern biochemistry. This was epitomized by the discovery of the double-helical structure of DNA, postulated by James Watson and Francis Crick in 1953 (see Fig. 8-15). Genetic theory contributed the concept of coding by genes. Physics permitted the determination of molecular structure by x-ray diffraction analysis. Chemistry revealed the composition of DNA. The profound impact of the Watson-Crick hypothesis arose from its ability to account for a wide range of observations derived from studies in these diverse disciplines.

This revolution in our understanding of the structure of DNA inevitably stimulated questions about its function. The double-helical structure itself clearly suggested how DNA might be copied so that the information it contains can be transmitted from one generation to the next. Clarification of how the information in DNA is converted into functional proteins came with the discovery of both messenger RNA and transfer RNA and with the deciphering of the genetic code.

These and other major advances gave rise to the central dogma of molecular biology, comprising the three major processes in the cellular utilization of genetic information. The first is **replication**, the copying of parental DNA to form daughter DNA molecules with identical nucleotide sequences. The second is **transcription**, the process by which parts of the genetic message encoded in DNA are copied precisely into RNA. The third is **translation**, whereby the genetic message encoded in messenger RNA is translated on the ribosomes into a polypeptide with a particular sequence of amino acids.



The central dogma of molecular biology, showing the general pathways of information flow via replication, transcription, and translation. The term "dogma" is a misnomer. Introduced by Francis Crick at a time when little evidence supported these ideas, the dogma has become a well-established principle.

Part III explores these and related processes. In Chapter 24 we examine the structure, topology, and packaging of chromosomes and genes. The processes underlying the central dogma are elaborated in Chapters 25 through 27. Finally, we turn to regulation, examining how the expression of genetic information is controlled (Chapter 28).

A major theme running through these chapters is the added complexity inherent in the biosynthesis of macromolecules that contain information. Assembling nucleic acids and proteins with particular sequences of nucleotides and amino acids represents nothing less than preserving the faithful expression of the template

upon which life itself is based. We might expect the formation of phosphodiester bonds in DNA or peptide bonds in proteins to be a trivial feat for cells, given the arsenal of enzymatic and chemical tools described in Part II. However, the framework of patterns and principles established in our examination of metabolic pathways thus far must be enlarged considerably to take into account molecular information. Bonds must be formed between *particular* subunits in informational biomolecules, avoiding either the occurrence or the persistence of sequence errors. This has an enormous impact on thermodynamics, chemistry, and enzymology of biosynthetic processes. Formation of a peptide bond requires an energy input of only about 21 kJ/mol of H_2O and can be catalyzed by relatively simple enzymes. To synthesize a bond between two specific amino acids at a particular point in a polypeptide, the cell invests about 125 kJ/mol while making use of more than 100 enzymes, RNA molecules, and specialized proteins. The chemistry involved in peptide bond formation does not change because of this requirement, but additional processes are layered over the basic reaction to ensure that the peptide bond is formed between particular amino acids. Information is expensive.

The dynamic interaction between nucleic acids and proteins is another central theme of Part III. With the important exception of a few catalytic RNA molecules (discussed in Chapters 26 and 27), the processes that make up the pathways of cellular information flow are catalyzed and regulated by proteins. An understanding of these enzymes and other proteins can have practical as well as intellectual rewards, because they form the basis of recombinant DNA technology (introduced in Chapter 9).